

said oligonucleotide does not comprise the iron response element, wherein said molecular interaction site is identified by a method comprising:

C100K  
comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said target nucleic acid;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

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39. (Amended) The oligonucleotide of claim 35 wherein said RNA of a selected organism is present in a eukaryotic cell.

C2  
40. (Amended) The oligonucleotide of claim 39 wherein said RNA of a selected organism is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

41. (Amended) The oligonucleotide of claim 35 wherein said RNA of a selected organism is present in a prokaryotic cell.

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C3  
51. (New Claim) An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the iron response element, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said target nucleic acid with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species, wherein said nucleotide sequence of said RNA of a selected organism is determined by assembling a plurality of expressed sequence tags;